

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/508,095

Source: O/PE

Date Processed by STIC: 9/7/2001

H16
RECEIVED
NOV 13 2001
TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>09/508,095</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic <input type="checkbox"/> Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	

AMC/MH - Biotechnology Systems Branch - 08/21/2001

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/508,095

DATE: 09/07/2001
 TIME: 14:23:53

Input Set : C:\Crf3\Datahold\09545199
 Output Set: N:\CRF3\09072001\I508095.raw

C--> 2 <140> CURRENT APPLICATION NUMBER: US/09/508,095
 C--> 2 <141> CURRENT FILING DATE: 2001-08-20
 W--> 2 <151> PRIOR FILING DATE: 1999-09-10
 W--> 0 <110> APPLICANT:
 W--> 0 <120> TITLE INVENTION:
 W--> 0 <130> FILE REFERENCE:
 4 <150> PRIOR APPLICATION NUMBER: 60/128,689
 5 <151> PRIOR FILING DATE: 1999-04-09
 7 <160> NUMBER OF SEQ ID NOS: 165
 9 <170> SOFTWARE: PatentIn Ver. 2.0

Does Not Comply
 Corrected Diskette Needed

<110>
 <120>
 <140>
 <141>
 <150>

These mandatory
 numeric identifiers
 and responses are missing
 corresponding to the
 indicated <151> line

ERRORED SEQUENCES

1952 <210> SEQ ID NO: 16
 1953 <211> LENGTH: 2110
 1954 <212> TYPE: PRT
 1955 <213> ORGANISM: Pasteurella multocida
 1957 <400> SEQUENCE: 16
 1958 Met Gln Pro Ala Gln Glu His Cys Gln Arg Ile Asn Asn Ile Val Asn
 1959 1 5 10 15
 1961 Gln Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala
 1962 20 25 30
 1964 Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu
 1965 35 40 45
 1967 Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn
 1968 50 55 60
 1970 Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg
 1971 65 70 75 80
 1973 Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn
 1974 85 90 95
 1976 Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala
 1977 100 105 110
 1979 Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser
 1980 115 120 125
 1982 Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys
 1983 130 135 140
 1985 Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala
 1986 145 150 155 160
 1988 Phe Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile
 1989 165 170 175
 1991 Thr Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser
 1992 180 185 190
 1994 Gly Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala
 1995 195 200 205
 1997 Leu Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu
 1998 210 215 220

(See
 item 12
 in Error
 summary
 sheet)

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Input Set : C:\Crf3\Datashold\09545199
Output Set: N:\CRF3\09072001\I508095.raw

2000 Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met
 2001 225 230 235 240
 2003 Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys
 2004 245 250 255
 2006 Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro
 2007 260 265 270
 2009 Thr Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly
 2010 275 280 285
 2012 Lys Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu
 2013 290 295 300
 2015 Arg Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser
 2016 305 310 315 320
 2018 Leu Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu
 2019 325 330 335
 2021 Glu Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met
 2022 340 345 350
 2024 Pro Asn Leu Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu
 2025 355 360 365
 2027 Ser Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile
 2028 370 375 380
 2030 Glu Glu Ser His Ser Asn Ser Asp Asp Val Leu Ser Met Asn Asp
 2031 385 390 395 400
 2033 Asp Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu
 2034 405 410 415
 2036 Lys Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly
 2037 420 425 430
 2039 Asn Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp
 2040 435 440 445
 2042 Glu Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu
 2043 450 455 460
 2045 Gly Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser
 2046 465 470 475 480
 2048 Thr Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys
 2049 485 490 495
 2051 Arg Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys
 2052 500 505 510
 2054 Leu Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln
 2055 515 520 525
 2057 Lys Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu
 2058 530 535 540
 2060 Lys Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp
 2061 545 550 555 560
 2063 Lys Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu
 2064 565 570 575
 2066 Glu Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu
 2067 580 585 590
 2069 Glu Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln
 2070 595 600 605
 2072 Ala Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu

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Input Set : C:\Crf3\Datahold\09545199
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2073	610	615	620
2075	Asp Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala		
2076	625	630	635
2078	Glu Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro		640
2079	645	650	655
2081	Lys Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn		
2082	660	665	670
2084	Gln Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu		
2085	675	680	685
2087	Asn Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe		
2088	690	695	700
2090	Asp His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His		
2091	705	710	715
2093	Leu Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu		720
2094	725	730	735
2096	Met Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly		
2097	740	745	750
2099	Ala Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val		
2100	755	760	765
2102	Trp Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys		
2103	770	775	780
2105	Val Tyr Phe Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly		
2106	785	790	795
2108	800	805	810
2109	Leu Gly Thr Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys		815
2111	Asp Val Val Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu		
2112	820	825	830
2114	Ala Ser Asn Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu		
2115	835	840	845
2117	Thr Arg Leu Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe		
2118	850	855	860
2120	Ala Asn Asp Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr		
2121	865	870	875
2123	880	885	890
2124	Glu Gly His Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val		895
2126	900	905	910
2129	Val Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys		
2130	915	920	925
2132	930	935	940
2135	Lys Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His		
2136	945	950	955
2138	960	965	970
2139	His Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys		975
2141	980	985	990
2144	Ala Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala		
2145	995	1000	1005

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2147 Gly Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu
 2148 1010 1015 1020
 2150 Phe Ala Ser Ala His Ala Ser Gly Gly Thr Ser Val Arg Tyr Asp
 E--> 2151 1025 1030 1035 1040
 2153 Tyr Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn
 2154 1045 1050 1055
 2156 His Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys
 2157 1060 1065 1070
 2159 Asp Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys
 2160 1075 1080 1085
 2162 His Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp
 2163 1090 1095 1100
 2165 Ile Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu
 E--> 2166 105 1105 1110 1115 1120
 2168 Ile Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val
 2169 1125 1130 1135
 2171 Ala Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro
 2172 1140 1145 1150
 2174 Glu Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu
 2175 1155 1160 1165
 2177 Lys Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala
 2178 1170 1175 1180
 2180 Pro Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser
 E--> 2181 185 1185 1190 1195 1200
 2183 Lys Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys
 2184 1205 1210 1215
 2186 Val Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser
 2187 1220 1225 1230
 2189 His Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp
 2190 1235 1240 1245
 2192 Gly Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr
 2193 1250 1255 1260
 2195 Gly Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His
 E--> 2196 265 1265 1270 1275 1280
 2198 Glu Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly
 2199 1285 1290 1295
 2201 Gly Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn
 2202 1300 1305 1310
 2204 Val Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp
 2205 1315 1320 1325
 2207 Val Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val
 2208 1330 1335 1340
 2210 Ser Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met
 E--> 2211 345 1345 1350 1355 1360
 2213 Ser Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu
 2214 1365 1370 1375
 2216 Ser Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys
 2217 1380 1385 1390
 2219 Ala Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser

When
 numbering
 first amino
 acid on a line,
 begin number
 under first
 letter of amino
 acid

l.g. Phe
 1025

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Input Set : C:\Crf3\Datahold\09545199
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2220 1395 1400 1405
 2222 Ser Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr
 2223 1410 1415 1420
 2225 Asn Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val
 E--> 2226 425 1430 1435 1440
 2228 Asp Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala
 2229 1445 1450 1455
 2231 Thr Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser
 2232 1460 1465 1470
 2234 Lys Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr
 2235 1475 1480 1485
 2237 Gly Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn
 2238 1490 1495 1500
 2240 Asp Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala
 E--> 2241 505 1510 1515 1520
 2243 Leu His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val
 2244 1525 1530 1535
 2246 Gly Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg
 2247 1540 1545 1550
 2249 Ala Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly
 2250 1555 1560 1565
 2252 Val Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu
 2253 1570 1575 1580
 2255 Thr Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln
 E--> 2256 585 1590 1595 1600
 2258 Phe Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys
 2259 1605 1610 1615
 2261 Asn Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser
 2262 1620 1625 1630
 2264 Thr Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr
 2265 1635 1640 1645
 2267 Arg Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro
 2268 1650 1655 1660
 2270 Ile Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn
 E--> 2271 665 1670 1675 1680
 2273 Val Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr
 2274 1685 1690 1695
 2276 Thr Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser
 2277 1700 1705 1710
 2279 Lys Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr
 2280 1715 1720 1725
 2282 Ser Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg
 2283 1730 1735 1740
 2285 Val Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr
 E--> 2286 745 1750 1755 1760
 2288 Thr Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp
 2289 1765 1770 1775
 2291 Pro Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp
 2292 1780 1785 1790

*Same
error*

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2294 Gly Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr
 2295 1795 1800 1805
 2297 Lys Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn
 2298 1810 1815 1820
 2300 Ala Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser
 E--> 2301 825 1830 1835 1840
 2303 Pro Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn
 2304 1845 1850 1855
 2306 Lys Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys
 2307 1860 1865 1870
 2309 Ala Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu
 2310 1875 1880 1885
 2312 Arg Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn
 2313 1890 1895 1900
 2315 Lys Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu
 E--> 2316 905 1910 1915 1920
 2318 Phe Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala
 2319 1925 1930 1935
 2321 Ile Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val
 2322 1940 1945 1950
 2324 Val Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala
 2325 1955 1960 1965
 2327 Pro Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp
 2328 1970 1975 1980
 2330 Ala Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg
 E--> 2331 985 1990 1995 2000
 2333 Arg Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys
 2334 2005 2010 2015
 2336 Gly Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala
 2337 2020 2025 2030
 2339 His Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn
 2340 2035 2040 2045
 2342 Gly Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu
 2343 2050 2055 2060
 2345 Val Glu Phe Asp Tyr Asn Asn His Leu Thr Pro Ser Phe Pro Gly Val
 E--> 2346 065 2070 2075 2080
 2348 Ile Ala Pro Leu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu
 2349 2085 2090 2095
 2351 Gly Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala
 2352 2100 2105 2110
 3855 <210> SEQ ID NO: 28
 3856 <211> LENGTH: 450
 3857 <212> TYPE: PRT
 3858 <213> ORGANISM: Pasteurella multocida
 3860 <400> SEQUENCE: 28
 3861 Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu
 3862 1 5 10 15
 3864 Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
 3865 20 25 30

P.7

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3867 Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
 3868 35 40 45
 3870 Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
 3871 50 55 60
 3873 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
 3874 65 70 75 80
 3876 Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
 3877 85 90 95
 3879 Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
 3880 100 105 110
 E--> 3882 Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
 3883 115 120 125
 E--> 3885 Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
 3886 130 135 140
 E--> 3888 Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
 3889 145 150 155 160
 3891 Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
 3892 165 170 175
 3894 Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Arg
 3895 180 185 190
 3897 Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
 3898 195 200 205
 3900 Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser
 3901 210 215 220
 3903 Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala
 3904 225 230 235 240
 3906 Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr
 3907 245 250 255
 3909 Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp
 3910 260 265 270
 3912 Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln
 3913 275 280 285
 3915 Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His
 3916 290 295 300
 3918 Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu
 3919 305 310 315 320
 3921 Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe
 3922 325 330 335
 3924 Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala
 3925 340 345 350
 3927 Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
 3928 355 360 365
 3930 Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
 3931 370 375 380
 3933 Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
 3934 385 390 395 400
 3936 Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
 3937 405 410 415
 3939 Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys

See item 9
 in Error
 Summary Sheet

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Input Set : C:\Crf3\Datahold\09545199
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3940 420 425 430
 3942 Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly
 3943 435 440 445
 3945 Gln Val
 3946 450
 5300 <210> SEQ ID NO: 36
 5301 <211> LENGTH: 302
 5302 <212> TYPE: PRT
 5303 <213> ORGANISM: Pasteurella multocida
 5305 <400> SEQUENCE: 36
 5306 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
 5307 1 5 10 15
 5309 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
 5310 20 25 30
 5312 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 5313 35 40 45
 5315 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 5316 50 55 60
 5318 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 5319 65 70 75 80
 5321 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
 5322 85 90 95
 5324 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
 5325 100 105 110
 5327 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
 5328 115 120 125
 5330 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
 5331 130 135 140
 5333 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
 5334 145 150 155 160
 5336 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
 5337 165 170 175
 5339 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
 5340 180 185 190
 5342 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
 5343 195 200 205
 E--> 5345 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly *item 9*
 5346 210 215 220
 E--> 5348 Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val *item 9*
 5349 225 230 235 240
 5351 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
 5352 245 250 255
 E--> 5354 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg *item 9*
 5355 260 265 270
 E--> 5357 Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala *item 9*
 5358 275 280 285
 5360 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
 5361 290 295 300
 5472 <210> SEQ ID NO: 38

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Input Set : C:\Crf3\Datashold\09545199
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5473 <211> LENGTH: 166
 5474 <212> TYPE: PRT
 5475 <213> ORGANISM: Pasteurella multocida
 5477 <400> SEQUENCE: 38
 5478 Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
 5479 1 5 10 15
 5481 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
 5482 20 25 30
 E--> 5484 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met *item 9*
 5485 35 40 45
 5487 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
 5488 50 55 60
 5490 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
 5491 65 70 75 80
 5493 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
 5494 85 90 95
 E--> 5496 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys *item 9*
 5497 100 105 110
 5499 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
 5500 115 120 125
 5502 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
 5503 130 135 140
 5505 Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
 5506 145 150 155 160
 5508 Cys Trp Cys Gly Cys Gly
 5509 165
 11512 <210> SEQ ID NO: 103
 11513 <211> LENGTH: 1643
 11514 <212> TYPE: PRT
 11515 <213> ORGANISM: Pasteurella multocida
 11517 <400> SEQUENCE: 103
 11518 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
 11519 1 5 10 15
 11521 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser
 11522 20 25 30
 11524 Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Pro Phe Leu
 11525 35 40 45
 11527 Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
 11528 50 55 60
 11530 Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
 11531 65 70 75 80
 11533 Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
 11534 85 90 95
 11536 Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile
 11537 100 105 110
 11539 Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
 11540 115 120 125
 11542 Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
 11543 130 135 140

β.13

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Input Set : C:\Crf3\Datahold\09545199
 Output Set: N:\CRF3\09072001\I508095.raw

11545 Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
 11546 145 150 155 160
 11548 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
 11549 165 170 175
 11551 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
 11552 180 185 190
 11554 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
 11555 195 200 205
 11557 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
 11558 210 215 220
 11560 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
 11561 225 230 235 240
 11563 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
 11564 245 250 255
 11566 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
 11567 260 265 270
 11569 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
 11570 275 280 285
 11572 Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
 11573 290 295 300
 11575 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
 11576 305 310 315 320
 11578 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
 11579 325 330 335
 11581 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
 11582 340 345 350
 11584 Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
 11585 355 360 365
 11587 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
 11588 370 375 380
 11590 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
 11591 385 390 395 400
 11593 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
 11594 405 410 415
 11596 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
 11597 420 425 430
 11599 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
 11600 435 440 445
 11602 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
 11603 450 455 460
 11605 Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
 11606 465 470 475 480
 11608 Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
 11609 485 490 495
 11611 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
 11612 500 505 510
 11614 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
 11615 515 520 525
 11617 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser

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Input Set : C:\Crf3\Datohold\09545199
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11618	530	535	540
11620	Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu		
11621	545	550	555
			560
11623	Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu		
11624	565	570	575
11626	Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn		
11627	580	585	590
11629	Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala		
11630	595	600	605
11632	Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr		
11633	610	615	620
11635	Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile		
11636	625	630	635
			640
11638	Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr		
11639	645	650	655
11641	Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn		
11642	660	665	670
11644	Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser		
11645	675	680	685
11647	Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His		
11648	690	695	700
11650	Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr		
11651	705	710	715
			720
11653	Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val		
11654	725	730	735
11656	His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu		
11657	740	745	750
11659	Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser		
11660	755	760	765
11662	Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser		
11663	770	775	780
11665	Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe		
11666	785	790	795
			800
11668	Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln		
11669	805	810	815
11671	Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr		
11672	820	825	830
11674	Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala		
11675	835	840	845
11677	Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly		
11678	850	855	860
11680	Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser		
11681	865	870	875
			880
11683	Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys		
11684	885	890	895
11686	Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp		
11687	900	905	910
11689	Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe		
11690	915	920	925

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Input Set : C:\Crf3\Datashold\09545199
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11692 Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
11693 930 935 940
11695 Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
11696 945 950 955 960
11698 Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
11699 965 970 975
11701 Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp
11702 980 985 990
11704 Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
11705 995 1000 1005
11707 Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile
11708 1010 1015 1020
11710 Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
11711 1025 1030 1035 1040
11713 His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser
11714 1045 1050 1055
11716 Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
11717 1060 1065 1070
11719 Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
11720 1075 1080 1085
11722 Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
11723 1090 1095 1100
11725 Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
11726 1105 1110 1115 1120
11728 Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
11729 1125 1130 1135
11731 Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
11732 1140 1145 1150
11734 Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
11735 1155 1160 1165
11737 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
11738 1170 1175 1180
11740 Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
11741 1185 1190 1195 1200
11743 Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
11744 1205 1210 1215
11746 Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
11747 1220 1225 1230
11749 Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Lys Lys
11750 1235 1240 1245
11752 Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
11753 1250 1255 1260
11755 Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
11756 1265 1270 1275 1280
11758 Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
11759 1285 1290 1295
11761 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
11762 1300 1305 1310
11764 Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp

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Input Set : C:\Crf3\Datohold\09545199
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11765	1315	1320	1325
11767	Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys		
11768	1330	1335	1340
11770	Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln		
11771	1345	1350	1355
11773	Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln		
11774	1365	1370	1375
11776	Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn		
11777	1380	1385	1390
11779	Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu		
11780	1395	1400	1405
11782	Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val		
11783	1410	1415	1420
11785	Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe		
11786	1425	1430	1435
11788	1440	1445	1450
11789	Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr		
11791	1455	1460	1465
11792	Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val		
11794	1470	1475	1480
11795	Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn		
11797	1485	1490	1495
11798	Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu		
11800	1500	1505	1510
11801	Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp		
11803	1520	1525	1530
11804	Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His		
11806	1535	1540	1545
11807	Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser		
11809	1550	1555	1560
11810	Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu		
11812	1565	1570	1575
11813	Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro		
11815	1580	1585	1590
11816	Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro		
11818	1600	1595	1605
11819	Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val		
E--> 11821	1615	Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa	
11822	1620	1625	1630
11824	1635	Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu	
11825	1640		

fyI →

Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/508,095

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Input Set : C:\Crf3\Datashold\09545199
Output Set: N:\CRF3\09072001\I508095.raw

L:2 M:270 C: Current Application Number differs, Replaced Current Application No
L:2 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2 M:289 W: Identifier Missing or Out-Of-Order, <150> PRIOR APP NO
L:0 M:201 W: Mandatory field data missing, APPLICANT NAME
L:0 M:201 W: Mandatory field data missing, TITLE INVENTION
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE
L:100 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:2151 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:16
M:332 Repeated in SeqNo=16
L:3766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3767 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3770 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3774 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:3882 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
M:340 Repeated in SeqNo=28
L:5261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5273 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5274 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5289 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5297 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35
L:5345 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
M:340 Repeated in SeqNo=36
L:5385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5386 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5401 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5433 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5435 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5461 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5463 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:5484 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:38
M:340 Repeated in SeqNo=38
L:5609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:39
L:6532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47
L:9085 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:72
L:10782 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:90
L:10782 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90
L:10782 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90
L:10784 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:90
L:10784 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:90
L:10784 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:90
L:11503 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:11504 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:102
L:11821 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103